



SEQUENCE LISTING

<110> Curtis, Rory A. J.

<120> 33410, A NOVEL HUMAN CARBOXYLESTERASE
FAMILY MEMBER AND USES THEREOF

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<141> 2001-08-21

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<210> 4

<211> 585

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence

<400> 4

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Asn Glu Lys Thr Asp Asn Gly Glu Gln Ser Val Tyr Ser Phe Leu Gly
      20             25             30
Ile Pro Tyr Ala Glu Pro Pro Val Gly Asn Leu Arg Phe Lys Ala Pro

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Pro	Pro	Ser	Cys	Leu	Gln	Asp	Asp	Asp	Phe	Gly	Phe	Ser	Leu	Ser	Asp	
65					70					75					80	
Leu	Lys	Val	Ala	Leu	Lys	Met	Leu	Ser	Leu	Gly	Trp	Asn	Lys	Leu	Val	
				85					90					95		
Gly	Leu	Lys	Leu	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Tyr	Thr	Pro	
			100					105					110			
Lys	Asn	Thr	Lys	Pro	Asn	Ser	Lys	Leu	Pro	Val	Met	Val	Trp	Ile	His	
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Tyr	Asp	Gly	Glu	Ser	Leu	Ala	Arg	Glu	Gly	Asn	Val	Ile	Val	Val	Ser	
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Ile	Asn	Tyr	Arg	Leu	Gly	Pro	Leu	Gly	Phe	Leu	Ser	Thr	Gly	Asp	Asp	
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Asn	Ser	Val	Thr	Ile	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ala	Ser	Val	Ser	
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Ala	Ile	Gln	Ser	Glu	Ser	Asn	Ala	Arg	Gly	Arg	Ala	Lys	Glu	Leu	Ala	
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Leu	Arg	Ser	Lys	Ser	Ala	Glu	Glu	Leu	Leu	Glu	Ala	Thr	Arg	Ser	Phe	
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Leu	Leu	Phe	Glu	Tyr	Val	Pro	Phe	Leu	Pro	Leu	Phe	Leu	Ala	Phe	Gly	
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Pro	Val	Val	Asp	Gly	Asp	Asp	Ala	Pro	Glu	Ala	Phe	Ile	Pro	Glu	Asp	
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Pro	Glu	Glu	Leu	Ile	Lys	Glu	Gly	Lys	Phe	Ala	Asp	Val	Pro	Tyr	Leu	
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Asn	Ala	Ser	Ser	Lys	Gly	Glu	Asp	Glu	Leu	Lys	Lys	Glu	Thr	Asn	Pro	
	370					375					380					
Asp	Val	Trp	Leu	Glu	Leu	Leu	Lys	Tyr	Leu	Leu	Phe	Tyr	Ala	Ser	Glu	
385					3											

Phe	Phe	Val	Phe	Gly	Asn	Pro	Leu	Leu	Lys	Glu	Gln	Leu	Tyr	Lys	Ala
			500					505					510		
Thr	Glu	Glu	Glu	Glu	Lys	Ser	Ser	Ser	Lys	Thr	Met	Met	Asn	Tyr	Trp
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	530					535					540				
Leu	Val	Val	Trp	Pro	Lys	Tyr	Thr	Ser	Glu	Glu	Gln	Lys	Tyr	Ser	Leu
545					550					555					560
Leu	Ile	Leu	Leu	Thr	Thr	Ile	Thr	Ala	Gln	Lys	Leu	Lys	Ala	Arg	Asp
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Pro	Arg	Lys	Val	Leu	Cys	Asn	Phe	Trp							
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<210> 5

<211> 836

<212> PRT

<213> Rattus norvegicus

<400> 5

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Leu	Gly	Ser	Leu	Gly	Glu	Glu	Arg	Phe	Pro	Val	Val	Asn	Thr	Ala	Tyr
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Gly	Arg	Val	Arg	Gly	Val	Arg	Arg	Glu	Leu	Asn	Asn	Glu	Ile	Leu	Gly
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Pro	Val	Val	Gln	Phe	Leu	Gly	Val	Pro	Tyr	Ala	Thr	Pro	Pro	Leu	Gly
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Ala	Arg	Arg	Phe	Gln	Pro	Pro	Glu	Ala	Pro	Ala	Ser	Trp	Pro	Gly	Val
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		100						105					110		
Ala	Leu	Pro	Ala	Ile	Met	Leu	Pro	Val	Trp	Phe	Thr	Asp	Asn	Leu	Glu
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Asn	Leu	Tyr	Val	Pro	Thr	Glu	Asp	Gly	Pro	Leu	Thr	Lys	Lys	Arg	Asp
145					150					155					160
Glu	Ala	Thr	Leu	Asn	Pro	Pro	Asp	Thr	Asp	Ile	Arg	Asp	Ser	Gly	Lys
				165					170					175	
Lys	Pro	Val	Met	Leu	Phe	Leu	His	Gly	Gly	Ser	Tyr	Met	Glu	Gly	Thr
			180					185					190		
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		195					200					205			
Val	Ala	Thr	Leu	Asn	Tyr	Arg	Leu	Gly	Val	Leu	Gly	Phe	Leu	Ser	Thr
	210					215					220				
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			245						250					255	
Glu	Arg	Ile	Thr	Ile	Phe	Gly	Ser	Gly	Ala	Gly	Ala	Ser	Cys	Val	Asn
			260					265					270		
Leu	Leu	Ile	Leu	Ser	His	His	Ser	Glu	Gly	Leu	Phe	Gln	Lys	Ala	Ile
		275					280					285			
Ala	Gln	Ser	Gly	Thr	Ala	Ile	Ser	Ser	Trp	Ser	Val	Asn	Tyr	Gln	Pro
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Leu	Lys	Tyr	Thr	Arg	Leu	Leu	Ala	Ala	Lys	Val	Gly	Cys	Asp	Arg	Glu
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Asp	Ser	Thr	Glu	Ala	Val	Glu	Cys	Leu	Arg	Arg	Lys	Ser	Ser	Arg	Glu
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Pro	Val	Val	Asp	Gly	Asp	Val	Val	Pro	Asp	Asp	Pro	Glu	Ile	Leu	Met
		355					360					365			
Gln	Gln	Gly	Glu	Phe	Leu	Asn	Tyr	Asp	Met	Leu	Ile	Gly	Val	Asn	Gln
	370					375					380				
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Val	Ser	Ala	Ser	Ala	Phe	Asp	Phe	Thr	Val	Ser	Asn	Phe	Val	Asp	Asn
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			420					425					430		
Phe	Met	Tyr	Thr	Asp	Trp	Ala	Asp	Arg	Asp	Asn	Gly	Glu	Met	Arg	Arg
		435					440					445			
Lys	Thr	Leu	Leu	Ala	Leu	Phe	Thr	Asp	His	Gln	Trp	Val	Ala	Pro	Ala
	450					455					460				
Val	Ala	Thr	Ala	Lys	Leu	His	Ala	Asp	Tyr	Gln	Ser	Pro	Val	Tyr	Phe
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Tyr	Thr	Phe	Tyr	His	His	Cys	Gln	Ala	Glu	Gly	Arg	Pro	Glu	Trp	Ala
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Asp	Ala	Ala	His	Gly	Asp	Glu	Leu	Pro	Tyr	Val	Phe	Gly	Val	Pro	Met
			500					505					510		
Val	Gly	Ala	Thr	Asp	Leu	Phe	Pro	Cys	Asn	Phe	Ser	Lys	Asn	Asp	Val
		515					520					525			
Met	Leu	Ser	Ala	Val	Val	Met	Thr	Tyr	Trp	Thr	Asn	Phe	Ala	Lys	Thr
	530					535					540				
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545					550					555					560
Lys	Pro	Asn	Arg	Phe	Glu	Glu	Val	Val	Trp	Ser	Lys	Phe	Asn	Ser	Lys
				565					570					575	
Glu	Lys	Gln	Tyr	Leu	His	Ile	Gly	Leu	Lys	Pro	Arg	Val	Arg	Asp	Asn
		580					585						590		
Tyr	Arg	Ala	Asn	Lys	Val	Ala	Phe	Trp	Leu	Glu	Leu	Val	Pro	His	Leu
		595					600					605			
His	Asn	Leu	His	Thr	Glu	Leu	Phe	Thr	Thr	Thr	Thr	Arg	Leu	Pro	Pro
	610					615					620				
Tyr	Ala	Thr	Arg	Trp	Pro	Pro	Arg	Thr	Pro	Gly	Pro	Gly	Thr	Ser	Gly
625					630					635					640
Thr	Arg	Arg	Pro	Pro	Pro	Pro	Ala	Thr	Leu	Pro	Pro	Glu	Ser	Asp	Ile
				645					650					655	
Asp	Leu	Gly	Pro	Arg	Ala	Tyr	Asp	Arg	Phe	Pro	Gly	Asp	Ser	Arg	Asp
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Tyr	Ser	Thr	Glu	Leu	Ser	Val	Thr	Val	Ala	Val	Gly	Ala	Ser	Leu	Leu
		675					680					685			
Phe	Leu	Asn	Ile	Leu	Ala	Phe	Ala	Ala	Leu	Tyr	Tyr	Lys	Arg	Asp	Arg
	690					695					700				
Arg	Gln	Glu	Leu	Arg	Cys	Arg	Arg	Leu	Ser	Pro	Pro	Gly	Gly	Ser	Gly
705					710					715					720
Ser	Gly	Val	Pro	Gly	Gly	Gly	Pro	Leu	Leu	Pro	Thr	Ala	Gly	Arg	Glu
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Leu	Pro	Pro	Glu	Glu	Glu	Leu	Val	Ser	Leu	Gln	Leu	Lys	Arg	Gly	Gly
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<211> 550
<212> PRT
<213> Homo sapiens
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Tyr	Gln	Pro	Leu 20	Lys	Tyr	Thr	Arg	Leu 25	Leu	Ala	Ala	Lys 30	Val	Gly	Cys	
Asp	Arg	Glu 35	Asp	Ser	Ala	Glu 40	Ala	Val	Glu	Cys	Leu 45	Arg	Arg	Lys	Pro	
Ser 50	Arg	Glu	Leu	Val	Asp 55	Gln	Asp	Val	Gln	Pro	Ala 60	Arg	Tyr	His	Ile	
Ala 65	Phe	Gly	Pro	Val	Val 70	Asp	Gly	Asp	Val	Val 75	Pro	Asp	Asp	Pro	Glu 80	
Ile	Leu	Met	Gln	Gln 85	Gly	Glu	Phe	Leu 90	Asn	Tyr	Asp	Met	Leu 95	Ile	Gly	
Val	Asn	Gln	Gly 100	Glu	Gly	Leu	Lys	Phe 105	Val	Glu	Asp	Ser	Ala 110	Glu	Ser	
Glu	Asp	Gly 115	Val	Ser	Ala	Ser	Ala 120	Phe	Asp	Phe	Thr	Val 125	Ser	Asn	Phe	
Val 130	Asp	Asn	Leu	Tyr	Gly 135	Tyr	Pro	Glu	Gly	Lys	Asp 140	Val	Leu	Arg	Glu	
Thr 145	Ile	Lys	Phe	Met	Tyr 150	Thr	Asp	Trp	Ala	Asp 155	Arg	Asp	Asn	Gly	Glu 160	
Met	Arg	Arg	Lys	Thr 165	Leu	Leu	Ala	Leu 170	Phe	Thr	Asp	His	Gln 175	Trp	Val	
Ala	Pro	Ala	Val 180	Ala	Thr	Ala	Lys	Leu 185	His	Ala	Asp	Tyr	Gln 190	Ser	Pro	
Val	Tyr	Phe 195	Tyr	Thr	Phe	Tyr	His 200	His	Cys	Gln	Ala	Glu 205	Gly	Arg	Pro	
Glu 210	Trp	Ala	Asp	Ala	Ala 215	His	Gly	Asp	Glu	Leu	Pro	Tyr 220	Val	Phe	Gly	
Val 225	Pro	Met	Val	Gly	Ala 230	Thr	Asp	Leu	Phe	Pro	Cys	Asn 235	Phe	Ser	Lys 240	
Asn	Asp	Val	Met	Leu 245	Ser	Ala	Val	Val 250	Met	Thr	Tyr	Trp	Thr	Asn	Phe 255	
Ala	Lys	Thr	Gly 260	Asp	Pro	Asn	Gln	Pro 265	Val	Pro	Gln	Asp	Thr	Lys	Phe	
Ile	His	Thr 275	Lys	Pro	Asn	Arg	Phe	Glu 280	Glu	Val	Val	Trp	Ser	Lys	Phe 285	
Asn	Ser	Lys	Glu	Lys	Gln 295	Tyr	Leu	His	Ile	Gly	Leu	Lys	Pro	Arg	Val 300	
Arg	Asp	Asn	Tyr	Arg	Ala	Asn	Lys	Val	Ala	Phe	Trp	Leu	Glu	Leu	Val	

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Pro His Leu His Asn Leu His Thr Glu Leu Phe Thr Thr Thr Thr Arg
          325          330          335
Leu Pro Pro Tyr Ala Thr Arg Trp Pro Pro Arg Pro Pro Ala Gly Ala
          340          345          350
Pro Gly Thr Arg Arg Pro Pro Pro Pro Ala Thr Leu Pro Pro Glu Pro
          355          360          365
Glu Pro Glu Pro Gly Pro Arg Ala Tyr Asp Arg Phe Pro Gly Asp Ser
          370          375          380
Arg Asp Tyr Ser Thr Glu Leu Ser Val Thr Val Ala Val Gly Ala Ser
385          390          395          400
Leu Leu Phe Leu Asn Ile Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Arg
          405          410          415
Asp Arg Arg Gln Glu Leu Arg Cys Arg Arg Leu Ser Pro Pro Gly Gly
          420          425          430
Ser Gly Ser Gly Val Pro Gly Gly Gly Pro Leu Leu Pro Ala Ala Gly
          435          440          445
Arg Glu Leu Pro Pro Glu Glu Glu Leu Val Ser Leu Gln Leu Lys Arg
          450          455          460
Gly Gly Gly Val Gly Ala Asp Pro Ala Glu Ala Leu Arg Pro Ala Cys
465          470          475          480
Pro Pro Asp Tyr Thr Leu Ala Leu Arg Arg Ala Pro Asp Asp Val Pro
          485          490          495
Leu Leu Ala Pro Gly Ala Leu Thr Leu Leu Pro Ser Gly Leu Gly Pro
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Pro Pro Pro Pro Pro Pro Pro Ser Leu His Pro Phe Gly Pro Phe Pro
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<210> 7

<211> 16

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<220>

<223> Exemplary motif

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<222> 2

<223> Xaa = Gly or Arg

<221> VARIANT

<222> 4-7, 9, 11, 13

<223> Xaa = Any amino acid

<221> VARIANT

<222> 8

<223> Xaa = Leu, Ile, Val, or Met

<221> VARIANT

<222> 10

<223> Xaa = Leu, Ile, or Val

<221> VARIANT

<222> 15

<223> Xaa = Ser, Thr, Ala, or Gly

<400> 7

Phe Xaa Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Ser Xaa Gly
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<210> 8

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Signature domain

<221> VARIANT

<222> 3, 7

<223> Xaa = any amino acid

<400> 8

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